

Rec'd PCT/PTO 25 MAR 2005
10/528183

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/528,183
Source: PG 10
Date Processed by STIC: 3/25/05

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PCT

RAW SEQUENCE LISTING

DATE: 03/25/2005

PATENT APPLICATION: US/10/528,183

TIME: 09:23:49

Input Set : A:\187203_1.txt

Output Set: N:\CRF4\03252005\J528183.raw

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4 <110> APPLICANT: Ullman, Katharine
5     Liu, Jin
6     Prunuske, Amy
7     Dimaano, Christian
9 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATED TO
10    INHIBITING NUCLEAR ENVELOPE BREAKDOWN
13 <130> FILE REFERENCE: 21101.0045U2
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/528,183
C--> 15 <141> CURRENT FILING DATE: 2005-03-17
15 <150> PRIOR APPLICATION NUMBER: PCT/US03/29267
16 <151> PRIOR FILING DATE: 2003-09-17
18 <150> PRIOR APPLICATION NUMBER: 60/411,248
19 <151> PRIOR FILING DATE: 2002-09-17
21 <160> NUMBER OF SEQ ID NOS: 35
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 5687
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
32     synthetic construct
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37 gggaggctct ctaaggcctc cgcctctgcc tctcccgccc ccttaccgcg cccggagcgg      180
38 gaagcgggcg aggtccgcc atggcctcgg gagccggagg agtcggaggg ggcgggtggcg      240
39 gcaagatccg gacgcggcgt tgccaccagg ggccaattaa gccttaccag caggggcgac      300
40 aacagcatca gggcattctt agcagggtta cagaatctgt taagaatatt gtgccagggt      360
41 ggctacaaag atacttcaac aagaatgaag atgtatgcag ctgttcaaca gacacaagcg      420
42 aggttccacg ctggccagaa aataaagagg accatctggt atatgccgat gaggagagct      480
43 ctaatattac tgatgggaga atcacacctg agccagcagt cagtaataca gaagaacctt      540
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50 ctgccttttg aacactttcc ccttcacttg ggaattcttc aatccttaaa accagtcagc      960
51 ttggagattc tcctttttat cctggaaaaa caacatacgg tggggcagca gctgctgtaa     1020
52 gacagtctaa actacgaaat acaccttatc aggcaccagt tagaagacaa atgaaagcta     1080
53 agcaactcag tgcacaatct tacggtgtga ccagttcaac agctcggcga atattgcagt     1140
54 ctttagagaa gatgtcaagc ctttagcgg atgcaaaaag aattccatcc attgtttctt     1200

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57	ccatagcaac	aaatcgaagt	gtttatttta	aaccatctct	gactccttct	ggtgaattca	1380
58	ggaagactaa	tcaaagaata	gataacaagt	gcagtactgg	atatgaaaaa	aatatgacac	1440
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60	cagccaatgg	tttatcttct	ggagtaggtg	gtggaggtgg	caagatgaga	cgagaaagaa	1560
61	cacgctttgt	tgcttctaaa	cctctggagg	aggaggaaat	ggaagttcca	gtattaccga	1620
62	aaatctctct	accgatcacc	agttcttcac	tgccctacct	taattttagt	tcccctgaga	1680
63	tcacaacttc	ctctccatca	cccatcaatt	cgtctcaagc	attaacaaac	aaggtacaaa	1740
64	tgacctctcc	gagcagcact	ggcagtccca	tgtttaaatt	ttcatctcca	atcgtaaaat	1800
65	ctactgaggc	aaatgtacta	cctccatcat	ctattggatt	tacatttagt	gtgcctgttg	1860
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67	ctcatcatgt	cactacagtg	aacagtacaa	attgtaagaa	gacaccacct	gaagattgtg	1980
68	agggctcttt	tgagcctgca	gaaatcctga	aagaagggaag	tgttctagat	attctgaaaa	2040
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70	cagtagttta	tacaagacca	gcaataagta	gcttttcttc	tagtggaatt	gggtttgggg	2160
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126 aaattgggga ttcttaaagt tgaatttatt ggcttttctg atccagtttt gtttgacca 5520
127 aaaaccagta ttgtacaaag tattaagcat atatttttat atttactaaa atggactgtg 5580
128 gtgacttttg ataataagga aaagtttaat attaaagcca tgtttattac agtataatta 5640
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133 <210> SEQ ID NO: 2

134 <211> LENGTH: 1475

135 <212> TYPE: PRT

136 <213> ORGANISM: Artificial Sequence

138 <220> FEATURE:

139 <223> OTHER INFORMATION: Description of Artificial Sequence: /note =
 140 synthetic construct

142 <400> SEQUENCE: 2

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145 Arg Thr Arg Arg Cys His Gln Gly Pro Ile Lys Pro Tyr Gln Gln Gly
146 20 25 30
147 Arg Gln Gln His Gln Gly Ile Leu Ser Arg Val Thr Glu Ser Val Lys
148 35 40 45
149 Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp
150 50 55 60
151 Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
152 65 70 75 80
153 Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
154 85 90 95
155 Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
156 100 105 110
157 Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg

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159 Pro Ser Leu His Arg Ser His Leu Asn Phe Ser Met Leu Glu Ser Pro
160          130          135          140
161 Ala Leu His Cys Gln Pro Ser Thr Ser Ser Ala Phe Pro Ile Gly Ser
162 145          150          155          160
163 Ser Gly Phe Ser Leu Val Lys Glu Ile Lys Asp Ser Thr Ser Gln His
164          165          170          175
165 Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser
166          180          185          190
167 Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp
168          195          200          205
169 Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr
170          210          215          220
171 Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser
172 225          230          235          240
173 Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp
174          245          250          255
175 Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala Ala
176          260          265          270
177 Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg
178          275          280          285
179 Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr
180          290          295          300
181 Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser
182 305          310          315          320
183 Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu
184          325          330          335
185 Asn Ser Pro Leu Asp Arg Ser Gly Ile Asp Ile Thr Asp Phe Gln Ala
186          340          345          350
187 Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met
188          355          360          365
189 Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys
190          370          375          380
191 Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile
192 385          390          395          400
193 Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln
194          405          410          415
195 Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu
196          420          425          430
197 Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Lys
198          435          440          445
199 Met Arg Arg Glu Arg Thr Arg Phe Val Ala Ser Lys Pro Leu Glu Glu
200          450          455          460
201 Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr
202 465          470          475          480
203 Ser Ser Ser Leu Pro Thr Phe Asn Phe Ser Ser Pro Glu Ile Thr Thr
204          485          490          495
205 Ser Ser Pro Ser Pro Ile Asn Ser Ser Gln Ala Leu Thr Asn Lys Val
206          500          505          510

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207 Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser
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209 Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser
210      530      535      540
211 Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser
212 545      550      555      560
213 Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His
214      565      570      575
215 Val Thr Thr Val Asn Ser Thr Asn Cys Lys Lys Thr Pro Pro Glu Asp
216      580      585      590
217 Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val
218      595      600      605
219 Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser
220      610      615      620
221 Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro
222 625      630      635      640
223 Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu
224      645      650      655
225 Lys Ala Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys
226      660      665      670
227 Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro
228      675      680      685
229 Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly
230      690      695      700
231 Lys Thr Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys
232 705      710      715      720
233 Pro Val Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys
234      725      730      735
235 Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr
236      740      745      750
237 Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu
238      755      760      765
239 Thr Met Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu
240      770      775      780
241 Gly Phe Gly Asp Lys Phe Lys Arg Pro Ile Gly Ser Trp Glu Cys Ser
242 785      790      795      800
243 Val Cys Cys Val Ser Asn Asn Ala Glu Asp Asn Lys Cys Val Ser Cys
244      805      810      815
245 Met Ser Glu Lys Pro Gly Ser Ser Val Pro Ala Ser Ser Ser Ser Thr
246      820      825      830
247 Val Pro Val Ser Leu Pro Ser Gly Gly Ser Leu Gly Leu Glu Lys Phe
248      835      840      845
249 Lys Lys Pro Glu Gly Ser Trp Asp Cys Glu Leu Cys Leu Val Gln Asn
250      850      855      860
251 Lys Ala Asp Ser Thr Lys Cys Leu Ala Cys Glu Ser Ala Lys Pro Gly
252 865      870      875      880
253 Thr Lys Ser Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Ser Asn
254      885      890      895
255 Ser Ala Ala Ser Ser Ser Phe Lys Phe Gly Val Ser Ser Ser Ser Ser

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date